

SEQUENCE LISTING

<110> Lees, Ann M.
 Lees, Robert S.
 Law, Simon W.
 Arjona, Anibal A.

<120> NOVEL LOW DENSITY LIPOPROTEIN BINDING
 PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ATHEROSCLEROSIS

<130> 10797-004001

<140> US 09/616,289

<141> 2000-07-14

<150> US 09/517,849

<151> 2000-03-02

<150> US 08/979,608

<151> 1997-11-26

<150> US 60/031,930

<151> 1996-11-27

<150> US 60/048,547

<151> 1997-06-03

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 151

<212> PRT

<213> Oryctolagus cuniculus

<400> 1

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Asp	Glu	Tyr	Asp	Glu	Asn	Lys	Phe	Val	Asp	Glu	Glu	Asp	Gly	Gly	Asp
			20					25						30	
Gly	Gln	Ala	Gly	Pro	Asp	Glu	Gly	Glu	Val	Asp	Ser	Cys	Leu	Arg	Gln
		35					40					45			
Gly	Asn	Met	Thr	Ala	Ala	Leu	Gln	Ala	Ala	Leu	Lys	Asn	Pro	Pro	Ile
	50				55					60					
Asn	Thr	Arg	Ser	Gln	Ala	Val	Lys	Asp	Arg	Ala	Gly	Ser	Ile	Val	Leu
65				70					75					80	
Lys	Val	Leu	Ile	Ser	Phe	Lys	Ala	Gly	Asp	Ile	Glu	Lys	Ala	Val	Gln
			85						90				95		
Ser	Leu	Asp	Arg	Asn	Gly	Val	Asp	Leu	Leu	Met	Lys	Tyr	Ile	Tyr	Lys
		100						105					110		
Gly	Phe	Glu	Ser	Pro	Ser	Asp	Asn	Ser	Ser	Ala	Val	Leu	Leu	Gln	Trp
	115					120						125			
His	Glu	Lys	Ala	Leu	Ala	Ala	Gly	Gly	Val	Gly	Ser	Ile	Val	Arg	Val
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10023529-12101

Leu Thr Ala Arg Lys Thr Val
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<210> 2
<211> 317
<212> PRT
<213> Oryctolagus cuniculus

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Tyr Leu Gly Gly Ser Ser Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg
35 40 45
Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu
50 55 60
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly
65 70 75 80
Arg Ala Pro Pro Ala Ala Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala
85 90 95
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Glu Glu Glu
100 105 110
Asp Asp Glu Asp Asp Asp Asp Val Val Ser Glu Gly Ser Glu Val
115 120 125
Pro Glu Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly
130 135 140
Gly Glu Arg Gly Pro Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser
145 150 155 160
Leu Cys Gly Pro His Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala
165 170 175
Gly Ser Gly Thr Arg Gln Val Phe Ser Met Ala Ala Leu Ser Lys Glu
180 185 190
Gly Gly Ser Ala Ser Ser Thr Thr Gly Pro Asp Ser Pro Ser Pro Val
195 200 205
Pro Leu Pro Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro
210 215 220
Phe Gly Cys Pro Ala Gly Arg Lys Glu Lys Pro Ala Asp Pro Val Glu
225 230 235 240
Trp Thr Val Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro
245 250 255
Glu Gln Ala Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu
260 265 270
Leu Leu Met Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu
275 280 285
Gly Pro Ala Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln
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Gly His Phe Glu Asp Asp Asp Pro Glu Gly Phe Leu Gly
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<211> 232

10023529-121701

<212> PRT

<213> *Oryctolagus cuniculus*

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 Leu Glu Lys Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp
 20 25 30
 Asp Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg
 35 40 45
 Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro
 50 55 60
 Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His
 65 70 75 80
 Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg
 85 90 95
 Gln Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser
 100 105 110
 Ser Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly
 115 120 125
 Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala
 130 135 140
 Gly Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp
 145 150 155 160
 Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala
 165 170 175
 Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg
 180 185 190
 Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys
 195 200 205
 Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp
 210 215 220
 Asp Asp Pro Glu Gly Phe Leu Gly
 225 230

<210> 4

<211> 252

<212> PRT

<213> *Oryctolagus cuniculus*

<400> 4

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 20 25 30
 Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Glu Glu Glu Asp
 35 40 45
 Asp Glu Asp Asp Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro
 50 55 60
 Glu Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Gly
 65 70 75 80
 Glu Arg Gly Pro Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu
 85 90 95
 Cys Gly Pro His Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly
 100 105 110
 Ser Gly Thr Arg Gln Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly
 115 120 125

FOXT 635200T

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<212> PRT
<213> Oryctolagus cuniculus
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Lys	Ser	Ser	Pro	Gly	Gln	Pro	Glu	Ala	Gly	Ala	Glu	Gly	Ala	Gln	Gly	
			20					25					30			
Arg	Pro	Gly	Arg	Pro	Ala	Pro	Ala	Arg	Glu	Ala	Glu	Gly	Ala	Ser	Ser	
		35					40					45				
Gln	Ala	Pro	Gly	Arg	Pro	Glu	Gly	Ala	Gln	Ala	Lys	Thr	Ala	Gln	Pro	
	50					55					60					
Gly	Ala	Leu	Cys	Asp	Val	Ser	Glu	Glu	Leu	Ser	Arg	Gln	Leu	Glu	Asp	
65				70						75					80	
Ile	Leu	Ser	Thr	Tyr	Cys	Val	Asp	Asn	Asn	Gln	Gly	Ala	Pro	Gly	Glu	
			85					90						95		
Asp	Gly	Val	Gln	Gly	Glu	Pro	Pro	Glu	Pro	Glu	Asp	Ala	Glu	Lys	Ser	
			100					105					110			
Arg	Ala	Tyr	Val	Ala	Arg	Asn	Gly	Glu	Pro	Glu	Pro	Gly	Thr	Pro	Val	
		115					120					125				
Val	Asn	Gly	Glu	Lys	Glu	Thr	Ser	Lys	Ala	Glu	Pro	Gly	Thr	Glu	Glu	
	130					135					140					
Ile	Arg	Thr	Ser	Asp	Glu	Val	Gly	Asp	Arg	Asp	His	Arg	Arg	Pro	Gln	
145				150						155					160	
Glu	Lys	Lys	Lys	Ala	Lys	Gly	Leu	Gly	Lys	Glu	Ile	Thr	Leu	Leu	Met	
			165						170					175		
Gln	Thr	Leu	Asn	Thr	Leu	Ser	Thr	Pro	Glu	Glu	Lys	Leu	Ala	Ala	Leu	
			180					185					190			
Cys	Lys	Lys	Tyr	Ala	Glu	Leu	Leu	Glu	Glu	His	Arg	Asn	Ser	Gln	Lys	
		195					200					205				
Gln	Met	Lys	Leu	Leu	Gln	Lys	Lys	Gln	Ser	Gln	Leu	Val	Gln	Glu	Lys	
	210					215					220					
Asp	His	Leu	Arg	Gly	Glu	His	Ser	Lys	Ala	Ile	Leu	Ala	Arg	Ser	Lys	
225				230						235					240	
Leu	Glu	Ser	Leu	Cys	Arg	Glu	Leu	Gln	Arg	His	Asn	Arg	Ser	Leu	Lys	
			245						250					255		
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<212> PRT
<213> Homo sapiens
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 His Glu Lys Ala Leu Ala Ala Gly Gly Val Gly Ser Ile Val Arg Val
 130 135 140
 Leu Thr Ala Arg Lys Thr Val
 145 150

<210> 7
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 7

Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu Asp
 1 5 10 15
 Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu Ser
 20 25 30
 Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg Gly
 35 40 45
 Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly Pro
 50 55 60
 His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly Thr
 65 70 75 80
 Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr Ala
 85 90 95
 Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro
 100 105 110
 Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro
 115 120 125
 Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val Met
 130 135 140
 Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr
 145 150 155 160
 Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln
 165 170 175
 Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu
 180 185 190
 Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu
 195 200 205
 Asp Asp Asp Pro Asp Gly Phe Leu Gly
 210 215

<210> 8
 <211> 530
 <212> PRT
 <213> Homo sapiens

<400> 8

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 Arg Pro Ser Gln Ala Ala Pro Ala Val Glu Ala Glu Gly Pro Gly Ser
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 Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala Gln
 35 40 45
 Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu Glu
 50 55 60
 Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro Gly

100235239 134301

65 70 75 80
 Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu Lys
 85 90 95
 Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro Val
 100 105 110
 Val Tyr Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu Glu
 115 120 125
 Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro Gln
 130 135 140
 Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu Met
 145 150 155 160
 Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu
 165 170 175
 Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser Gln Lys
 180 185 190
 Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys
 195 200 205
 Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys
 210 215 220
 Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys
 225 230 235 240
 Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys Glu
 245 250 255
 Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met
 260 265 270
 Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu
 275 280 285
 Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu
 290 295 300
 Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu
 305 310 315 320
 Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu
 325 330 335
 Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu
 340 345 350
 Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys
 355 360 365
 Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr
 370 375 380
 Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu
 385 390 395 400
 Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr
 405 410 415
 Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu
 420 425 430
 Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile
 435 440 445
 Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp
 450 455 460
 Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu
 465 470 475 480
 Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala
 485 490 495
 Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala Pro
 500 505 510
 Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser Ala
 515 520 525

10023529-12701

Arg Ala
530

<210> 9
<211> 20
<212> PRT
<213> Homo sapiens

<400> 9
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1 5 10 15
Gly Gly Asp Gly
20

<210> 10
<211> 1404
<212> DNA
<213> Oryctolagus cuniculus

<220>
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<222> (58)...(510)

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Ser Lys Asn Thr Val Ser Ser Ala Arg Phe Arg Lys Val Asp Val Asp
5 10 15

gag tac gac gag aac aag ttc gtg gac gag gaa gac ggc ggc gac ggc 156
Glu Tyr Asp Glu Asn Lys Phe Val Asp Glu Glu Asp Gly Gly Asp Gly
20 25 30

cag gcg ggg ccg gac gag ggc gag gtg gac tcg tgc ctg cgg caa ggg 204
Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser Cys Leu Arg Gln Gly
35 40 45

aac atg aca gcc gcc ctg cag gcg gcg ctg aag aac cct ccc atc aac 252
Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys Asn Pro Pro Ile Asn
50 55 60 65

acc agg agc cag gcg gtg aag gac cgg gca ggc agc atc gtg ctg aag 300
Thr Arg Ser Gln Ala Val Lys Asp Arg Ala Gly Ser Ile Val Leu Lys
70 75 80

gtg ctc atc tcc ttc aag gcc ggc gac ata gaa aag gcc gtg cag tcc 348
Val Leu Ile Ser Phe Lys Ala Gly Asp Ile Glu Lys Ala Val Gln Ser
85 90 95

ctg gac agg aac ggc gtg gac ctg ctc atg aag tac atc tac aag ggc 396
Leu Asp Arg Asn Gly Val Asp Leu Leu Met Lys Tyr Ile Tyr Lys Gly
100 105 110

ttc gag agc ccc tcc gac aac agc agc gcc gtg ctc ctg cag tgg cac 444

1002529 14301

Phe Glu Ser Pro Ser Asp Asn Ser Ser Ala Val Leu Leu Gln Trp His
 115 120 125

gag aag gcg ctg gct gca gga gga gtg ggc tcc atc gtc cgt gtc ctg 492
 Glu Lys Ala Leu Ala Ala Gly Gly Val Gly Ser Ile Val Arg Val Leu
 130 135 140 145

act gca agg aaa acc gtg tagcctggca ggaacgggtg cctgccgggg 540
 Thr Ala Arg Lys Thr Val
 150

agcgggagct gccggtacaa agacccaaaac gccagatgc cgccgctgcc ctgtgggagg 600
 cgtctgttcc cagcttcgct ttttcccttt cccgtgtctg tcaggattac ataagggtttc 660
 ccttcgtgag aatcggagtgc gcgcagaggg tcctgttcat acgcgccgtg cgtccgggtg 720
 tgtaagaccc ctgccttcag tgcctttag caacggtagc gtgtcgccgg ctgggttttg 780
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 ctcttccctt atttaagcag agtgagtgtt tggaaccagt ggtgcccccc cccccgcccc 960
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 gagcacactg gttctcagaa cacggccggc gcttgacggt tgtcacagct ccagaacaaa 1260
 tcctgggaga cagggcagcg cgagtcgccg ggcaggaatt ccacacactc gtgctgtttt 1320
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<210> 11
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 <212> DNA
 <213> Oryctolagus cuniculus

<220>
 <221> CDS
 <222> (1) ... (951)

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cgg gcc ggc ggc ccg gcg cgg ccc gtg agc ctg cgg gaa gtc gtg cgc 96
 Arg Ala Gly Gly Pro Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg
 20 25 30

tac ctc ggg ggt agc agc ggc gct ggc ggc cgc ctg acc cgc ggc cgc 144
 Tyr Leu Gly Gly Ser Ser Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg
 35 40 45

gtg cag ggt ctg ctg gaa gag gag gcg gcg gcg cgg ggc cgc ctg gag 192
 Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu
 50 55 60

cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga 240
 Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly
 65 70 75

10023529 121701

cgg gcg cca ccg gcc gcc agc gcc cgc gcg gcg cgg aac aag aga gct 288
 Arg Ala Pro Pro Ala Ala Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala
 80 85 90 95
 ggc gag gag cga gtg ctt gaa aag gag gag gag gag gag gag gag gaa 336
 Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu
 100 105 110
 gac gac gag gac gac gac gac gac gtc gtg tcc gag ggc tcg gag gtg 384
 Asp Asp Glu Asp Asp Asp Asp Asp Val Val Ser Glu Gly Ser Glu Val
 115 120 125
 ccc gag agc gat cgt ccc gcg ggt gcg cag cat cac cag ctg aat ggc 432
 Pro Glu Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly
 130 135 140
 ggc gag cgc ggc ccg cag acc gcc aag gag cgg gcc aag gag tgg tcg 480
 Gly Glu Arg Gly Pro Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser
 145 150 155
 ctg tgt ggc ccc cac cct ggc cag gag gaa ggg cgg ggg ccg gcc gcg 528
 Leu Cys Gly Pro His Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala
 160 165 170 175
 ggc agt ggc acc cgc cag gtg ttc tcc atg gcg gcc ttg agt aag gag 576
 Gly Ser Gly Thr Arg Gln Val Phe Ser Met Ala Ala Leu Ser Lys Glu
 180 185 190
 ggg gga tca gcc tct tcg acc acc ggg cct gac tcc ccg tcc ccg gtg 624
 Gly Gly Ser Ala Ser Ser Thr Thr Gly Pro Asp Ser Pro Ser Pro Val
 195 200 205
 cct ttg ccc ccc ggg aag cca gcc ctc cca gga gcc gat ggg acc ccc 672
 Pro Leu Pro Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro
 210 215 220
 ttt ggc tgc cct gcc ggg cgc aaa gag aag ccg gca gac ccc gtg gag 720
 Phe Gly Cys Pro Ala Gly Arg Lys Glu Lys Pro Ala Asp Pro Val Glu
 225 230 235
 tgg aca gtc atg gac gtc gtg gag tac ttc acc gag gcg ggc ttc cct 768
 Trp Thr Val Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro
 240 245 250 255
 gag caa gcc acg gct ttc cag gag cag gag atc gac ggc aag tcc ctg 816
 Glu Gln Ala Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu
 260 265 270
 ctg ctc atg cag cgc acc gat gtc ctc acc ggc ctg tcc atc cgc ctg 864
 Leu Leu Met Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu
 275 280 285
 ggg cca gcg ttg aaa atc tat gag cac cat atc aag gtg ctg cag cag 912
 Gly Pro Ala Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln
 290 295 300
 ggt cac ttc gag gac gat gac ccg gaa ggc ttc ctg gga tgagcacaga 961

T003E29-10701

Gly His Phe Glu Asp Asp Asp Pro Glu Gly Phe Leu Gly
305 310 315

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gattctggta	gggggcgggg	ccttgctgtg	ctcattgcta	ccccccacc	ccgtgtgtgt	1141
ctctgcacct	gccccagca	caccctccc	ggagcctgga	tgtcgctgg	gactctggcc	1201
tgctcatttt	gccccagat	cagccccctc	cctccctcct	gtcccaggac	attttttaaa	1261
agaaaaaaag	gaaaaaaaaa	aattggggag	ggggctggga	aggtgcccc	agatcctcct	1321
cggcccaacc	agggtgttat	tctatatat	atatatatat	gtttgtttct	gcctgttttt	1381
cgttttttgg	tgcgtggcct	tcttccctc	ccaccaccac	tcattggcccc	agccttgcct	1441
gccctgtcgg	cgggagcagc	tgggaatggg	aggaggggtg	gaccttgggt	gtctctccca	1501
ccctctctcc	cgttggttct	gttgctgctc	cagctggctg	tattgctttt	taatatgtca	1561
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<210> 12

<211> 1362

<212> DNA

<213> *Oryctolagus cuniculus*

$\langle 220 \rangle$

<221> CDS

<222> (1) ... (696)

<400> 12

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1 5 10 15

ctt gaa aag gag gag gag gag gag gag gag gaa gac gac gag gac gac 96
Leu Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp
20 25 30

gac gac gac gtc gtg tcc gag ggc tcg gag gtg ccc gag agc gat cgt 144
Asp Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg
35 40 45

ccc gcg ggt gcg cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg 192
Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro
50 55 60

cag acc gcc aag gag cgg gcc aag gag tgg tcg ctg tgt ggc ccc cac 240
Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His
65 70 75 80

cct ggc cag gag gaa ggg cgg ggg ccg gcc gcg ggc agt ggc acc cgc 288
Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg
85 90 95

cag gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct 336
Gln Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser
100 105 110

tcg acc acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg 384
Ser Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly
115 120 125

[illegible]

aag cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc 432
 Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala
 130 135 140

ggg cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac 480
 Gly Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp
 145 150 155 160

gtc gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct 528
 Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala
 165 170 175

ttc cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc 576
 Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg
 180 185 190

acc gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa 624
 Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys
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 Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp
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 Asp Asp Pro Glu Gly Phe Leu Gly
 225 230

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1003529-12101

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gag cgc ggc ccg cag acc gcc aag gag cgg gcc aag gag tgg tcg ctg Glu Arg Gly Pro Gln Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu 85 90 95	288
tgt ggc ccc cac cct ggc cag gag gaa ggg cgg ggg ccg gcc gcg ggc Cys Gly Pro His Pro Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly 100 105 110	336
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10023539 121701

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<400> 14

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Met Lys Asn Gln Asp Lys Lys Asn Gly Ala Ala Lys Gln Pro Asn Pro
1 5 10 15

aaa agc agc ccg gga cag ccg gaa gca gga gcg gag gga gcc cag ggg 156
Lys Ser Ser Pro Gly Gln Pro Glu Ala Gly Ala Glu Gly Ala Gln Gly
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cgg ccc ggc cgg ccg gcc ccc gcc cga gaa gcc gaa ggt gcc agc agc 204
Arg Pro Gly Arg Pro Ala Pro Ala Arg Glu Ala Glu Gly Ala Ser Ser
35 40 45

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Gln Ala Pro Gly Arg Pro Glu Gly Ala Gln Ala Lys Thr Ala Gln Pro
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Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Ala Pro Gly Glu
85 90 95

gat ggg gtc cag ggt gag ccc cct gaa cct gaa gat gca gag aag tct 396
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100 105 110

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Val Asn Gly Glu Lys Glu Thr Ser Lys Ala Glu Pro Gly Thr Glu Glu

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tgc aag aag tat gcg gaa ctg ctc gag gag cac cgg aac tcg cag aag Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser Gln Lys 195 200 205			684
cag atg aag ctg ctg cag aag aag cag agc cag ctg gtg cag gag aag Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys 210 215 220			732
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Met
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Glu Tyr Asp Glu Asn Lys Phe Val Asp Glu Glu Asp Gly Gly Asp Gly	
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cag gcc ggg ccc gac gag ggc gag gtg gac tcc tgc ctg cgg caa gga	264
Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser Cys Leu Arg Gln Gly	
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aac atg aca gct gcc cta cag gca gct ctg aag aac ccc cct atc aac	312
Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys Asn Pro Pro Ile Asn	
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acc aag agt cag gca gtg aag gac cgg gca ggc agc att gtc ttg aag	360
Thr Lys Ser Gln Ala Val Lys Asp Arg Ala Gly Ser Ile Val Leu Lys	
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Val Leu Ile Ser Phe Lys Ala Asn Asp Ile Glu Lys Ala Val Gln Ser	
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 Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu Ser
 20 25 30

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 Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg Gly
 35 40 45

cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga ccg 192
 Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly Pro
 50 55 60

cac cag ggc cag gat gaa ggg cgg ggg cca gcc ccg ggc agc ggc acc 240
 His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly Thr
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165 170 175

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Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu
180 185 190

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Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu
195 200 205

gat gat gac ccc gat ggc ttc tta ggc tgagcgccca gcctcaccac 671
Asp Asp Asp Pro Asp Gly Phe Leu Gly
210 215

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Glu Arg Pro Ser Gln Ala Ala Pro Ala Val Glu Ala Glu Gly Pro Gly
20 25 30

agc agc cag gct cct cgg aag ccg gag ggg gct caa gcc aga acg gct 143
Ser Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala
35 40 45

cag tct ggg gcc ctt cgt gat gtc tct gag gag ctg agc cgc caa ctg 191
Gln Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu
50 55 60

gaa gac ata ctg agc aca tac tgt gtg gac aat aac cag ggg ggc ccc 239
Glu Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro
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 Gly Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu
 80 85 90 95
 aag tcc cgg acc tat gtg gca agg aat ggg gag cct gaa cca act cca 335
 Lys Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro
 100 105 110
 gta gtc tat gga gag aag gaa ccc tcc aag ggg gat cca aac aca gaa 383
 Val Val Tyr Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu
 115 120 125
 gag atc cgg cag agt gac gag gtc gga gac cga gac cat cga agg cca 431
 Glu Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro
 130 135 140
 cag gag aag aaa aaa gcc aag ggt ttg ggg aag gag atc acg ttg ctg 479
 Gln Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu
 145 150 155
 atg cag aca ttg aat act ctg agt acc cca gag gag aag ctg gct gct 527
 Met Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala
 160 165 170 175
 ctg tgc aag aag tat gct gaa ctg ctg gag gag cac cgg aat tca cag 575
 Leu Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser Gln
 180 185 190
 aag cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag 623
 Lys Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu
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 aag gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc 671
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 210 215 220
 aag ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc 719
 Lys Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu
 225 230 235
 aag gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag 767
 Lys Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys
 240 245 250 255
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 Glu Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln
 260 265 270
 atg gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg 863
 Met Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met
 275 280 285
 gag ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc 911
 Glu Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg
 290 295 300
 gag gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag 959

10023529 1E1701

Glu Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln
 305 310 315
 ctg gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca 1007
 Leu Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala
 320 325 330 335
 gaa gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta 1055
 Glu Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val
 340 345 350
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 Glu Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu
 355 360 365
 aag caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac 1151
 Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn
 370 375 380
 aca ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg 1199
 Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met
 385 390 395
 gaa aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg 1247
 Glu Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met
 400 405 410 415
 tac cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct 1295
 Tyr Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala
 420 425 430
 gag gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa 1343
 Glu Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys
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 480 485 490 495
 gca ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca 1535
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 Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser
 515 520 525
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10023529 121701

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ggc ggc gac ggc 60
 Gly Gly Asp Gly
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<400> 19
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 1 5 10 15

<210> 20
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 20
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 1 5 10 15
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 20 25

<210> 21
 <211> 11
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<400> 21
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 1 5 10

<210> 22
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<400> 22
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 1 5 10

<210> 23
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<212> PRT
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<400> 23
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 20 25 30

<210> 24
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 <212> PRT
 <213> Oryctolagus cuniculus

<400> 24
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 1 5

<210> 25
 <211> 16
 <212> PRT
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 1 5 10 15

<210> 26
 <211> 28
 <212> PRT
 <213> Oryctolagus cuniculus

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 Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp
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<210> 27
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<400> 27
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 1 5 10

<210> 28
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<400> 28
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 1 5 10

<210> 29

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<211> 15
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 1 5 10 15

<210> 30
 <211> 45
 <212> DNA
 <213> Homo sapiens

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<210> 31
 <211> 78
 <212> DNA
 <213> Homo sapiens

<400> 31
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 gaagtgtccc agagtgtgac 78

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 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 32
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<210> 33
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 33
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<210> 34
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 <212> DNA
 <213> Homo sapiens

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 caggccgggg cgcacgaggg cgaggtggac 90

<210> 35
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 35
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1003554.2170

<210> 36
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 <400> 36
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 <210> 37
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 <210> 42
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 <212> DNA
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 <400> 42

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<210> 43

<211> 538

<212> PRT

<213> Homo sapiens

<400> 43

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 35 40 45
 Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro
 50 55 60
 Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg
 65 70 75 80
 Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala
 85 90 95
 Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro
 100 105 110
 Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Pro Pro
 115 120 125
 Pro Thr Pro Ala Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala
 130 135 140
 Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Thr Ala Pro Pro
 145 150 155 160
 Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro
 165 170 175
 Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro
 180 185 190
 Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu
 195 200 205
 Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln
 210 215 220
 Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val
 225 230 235 240
 Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg
 245 250 255
 Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg
 260 265 270
 Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu
 275 280 285
 Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly
 290 295 300
 Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly
 305 310 315 320
 Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu
 325 330 335
 Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu
 340 345 350
 Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg
 355 360 365
 Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly
 370 375 380
 Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly

10023529 121701

385 390 395 400
 Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr
 405 410 415
 Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro
 420 425 430
 Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys
 435 440 445
 Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val
 450 455 460
 Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala
 465 470 475 480
 Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met
 485 490 495
 Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala
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 <212> PRT
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 35 40 45
 Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala Gln
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 Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu Glu
 65 70 75 80
 Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro Gly
 85 90 95
 Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu Lys
 100 105 110
 Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro Val
 115 120 125
 Val Asn Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu Glu
 130 135 140
 Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro Gln
 145 150 155 160
 Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu Met
 165 170 175
 Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu
 180 185 190
 Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser Gln Lys
 195 200 205
 Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys
 210 215 220
 Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys
 225 230 235 240
 Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys

10023529.121701

245 250 255
 Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Lys Arg Lys Glu
 260 265 270
 Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met
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 Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu
 290 295 300
 Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu
 305 310 315 320
 Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu
 325 330 335
 Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu
 340 345 350
 Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu
 355 360 365
 Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys
 370 375 380
 Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr
 385 390 395 400
 Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu
 405 410 415
 Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr
 420 425 430
 Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu
 435 440 445
 Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile
 450 455 460
 Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp
 465 470 475 480
 Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu
 485 490 495
 Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala
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48

acc acg gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa
 Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His Tyr Gln
 20 25 30

96

10033529 161701

gag tgg atc ctg gac acc atc gac tgc ctg cgc tgc cgc aag gcg cgg	144
Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg	
35 40 45	
ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgc cac ggc ccg	192
Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro	
50 55 60	
gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag cag cgc	240
Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg	
65 70 75 80	
gcc gtg ctc cgg gtc agc tac aag ggg agc atc tgc tac cgc aac gcg	288
Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala	
85 90 95	
gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc ccg ccg	336
Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro	
100 105 110	
cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcc gcc ccg ccg	384
Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc	432
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc aca gcg ccc ccc	480
Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Thr Ala Pro Pro	
145 150 155 160	
tgc cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg gcc gcg ccc	528
Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro	
165 170 175	
ctg gcc gcg ccg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc	576
Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro	
180 185 190	
ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc ccg gag	624
Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu	
195 200 205	
ccg ccg ctg ccg ccg ccg cca cag ccg ccg gcg ccg cca cag cag cag	672
Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln	
210 215 220	
cag ccg ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg gtg	720
Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val	
225 230 235 240	
cgg gcc ggc ggc gcg gcg cgg ccc gtg agc ctg cgg gaa gtc gtg cgc	768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg	
245 250 255	

10023529-121701

tac ctc ggg ggc agc ggc ggc gcc ggc ggt cgc cta acc cgc ggc cgc Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg 260 265 270	816
gtg cag ggg ctg ctg gag gag gag gcg gcg gct cga ggc cgt ctg gag Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu 275 280 285	864
cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly 290 295 300	912
cgg gcg ccg ccg gcc gcc agc gcc cgc ccg tct cgc agc aag aga ggt Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly 305 310 315 320	960
gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu 325 330 335	1008
gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu 340 345 350	1056
agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag cgg Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg 355 360 365	1104
gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly 370 375 380	1152
ccg cac cag ggc cag gat gaa ggg cgg ggg cca gcc ccg ggc agc ggc Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly 385 390 395 400	1200
acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr 405 410 415	1248
gct tct gtt gcc acc ggg cca gac tcc ccg tcc ccc gtg cct ttg ccc Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro 420 425 430	1296
cca ggc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys 435 440 445	1344
ccg ccc ggg cgc aaa gag aag cca tct gat ccc gtc gag tgg acc gtg Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val 450 455 460	1392
atg gat gtc gtc gaa tat ttt act gag gct gga ttc ccg gag cag gcg Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala 465 470 475 480	1440
aca gct ttc caa gag cag gaa att gat ggc aaa tct ttg ctg ctc atg	1488

T027E1 "625200F

Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met
485 490 495

cag cgc aca gat gtg ctc acc ggc ctg tcc atc cgc ctc ggg cca gcc 1536
Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala
500 505 510

ctg aaa atc tac gag cac cac atc aag gtg ctt cag caa ggc cac ttt 1584
Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe
515 520 525

gag gat gat gac ccc gat ggc ttc tta ggc 1614
Glu Asp Asp Asp Pro Asp Gly Phe Leu Gly
530 535

<210> 46
<211> 1638
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1638)

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Met Lys Asn Gln Asp Lys Lys Asn Gly Ala Ala Lys Gln Ser Asn Pro
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aaa agc agc cca gga caa ccg gaa gca gga ccc gag gga gcc cag gag 96
Lys Ser Ser Pro Gly Gln Pro Glu Ala Gly Pro Glu Gly Ala Gln Glu
20 25 30

cgg ccc agc cag gcg gct cct gca gta gaa gca gaa ggt ccc ggc agc 144
Arg Pro Ser Gln Ala Ala Pro Ala Val Glu Ala Glu Gly Pro Gly Ser
35 40 45

agc cag gct cct cgg aag ccg gag ggt gct caa gcc aga acg gct cag 192
Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala Gln
50 55 60

tct ggg gcc ctt cgt gat gtc tct gag gag ctg agc cgc caa ctg gaa 240
Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu Glu
65 70 75 80

gac ata ctg agc aca tac tgt gtg gac aat aac cag ggg ggc ccc ggc 288
Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro Gly
85 90 95

gag gat ggg gca cag ggt gag ccg gct gaa ccc gaa gat gca gag aag 336
Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu Lys
100 105 110

tcc cgg acc tat gtg gca agg aat ggg gag cct gaa cca act cca gta 384
Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro Val
115 120 125

10035501 12101

gtc aat gga gag aag gaa ccc tcc aag ggg gat cca aac aca gaa gag Val Asn Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu Glu 130 135 140	432
atc cgg cag agt gac gag gtc gga gac cga gac cat cga agg cca cag Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro Gln 145 150 155 160	480
gag aag aaa aaa gcc aag ggt ttg ggt aag gag atc acg ttg ctg atg Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu Met 165 170 175	528
cag aca ttg aat act ctg agt acc cca gag gag aag ctg gct gct ctg Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu 180 185 190	576
tgc aag aag tat gct gaa ctg ctg gag gag cac cgg aat tca cag aag Cys Lys Lys Tyr Ala Glu Leu Glu Glu His Arg Asn Ser Gln Lys 195 200 205	624
cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag aag Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys 210 215 220	672
gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc aag Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys 225 230 235 240	720
ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc aag Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys 245 250 255	768
gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag gag Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys Glu 260 265 270	816
gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag atg Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met 275 280 285	864
gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg gag Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu 290 295 300	912
ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc gag Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu 305 310 315 320	960
gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag ctg Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu 325 330 335	1008
gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca gaa Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu 340 345 350	1056

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gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta gag 1104
 Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu
 355 360 365

 tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg aag 1152
 Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys
 370 375 380

 caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac aca 1200
 Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr
 385 390 395 400

 ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg gaa 1248
 Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu
 405 410 415

 aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg tac 1296
 Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr
 420 425 430

 cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct gag 1344
 Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu
 435 440 445

 gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa atc 1392
 Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile
 450 455 460

 caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat gac 1440
 Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp
 465 470 475 480

 ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc ctc 1488
 Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu
 485 490 495

 act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa gca 1536
 Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala
 500 505 510

 ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca ccg 1584
 Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala Pro
 515 520 525

 agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc gcc 1632
 Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser Ala
 530 535 540

 agg gcc 1638
 Arg Ala
 545

<210> 47

<211> 550

<212> PRT

<213> *Oryctolagus cuniculus*

10023529 104701
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<400> 47

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 Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala
 35 40 45
 Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly
 50 55 60
 Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln
 65 70 75 80
 Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn
 85 90 95
 Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro
 100 105 110
 Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Pro Pro Pro
 115 120 125
 Thr Pro Ala Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala
 130 135 140
 Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Thr Ala
 145 150 155 160
 Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala
 165 170 175
 Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Ala
 180 185 190
 Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala Val
 195 200 205
 Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro
 210 215 220
 Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Gln Gln Pro
 225 230 235 240
 Gln Pro Pro Pro Glu Gly Gly Ala Ala Arg Ala Gly Gly Pro Ala Arg
 245 250 255
 Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser Gly
 260 265 270
 Ala Gly Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu Glu
 275 280 285
 Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala Leu
 290 295 300
 Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala Ser
 305 310 315 320
 Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu Glu
 325 330 335
 Lys Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp Asp
 340 345 350
 Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro Ala
 355 360 365
 Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln Thr
 370 375 380
 Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro Gly
 385 390 395 400
 Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln Val
 405 410 415
 Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser Thr
 420 425 430
 Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys Pro

10023529 121701

435 440 445
 Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly Arg
 450 455 460
 Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val Val
 465 470 475 480
 Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe Gln
 485 490 495
 Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr Asp
 500 505 510
 Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile Tyr
 515 520 525
 Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp Asp
 530 535 540
 Pro Glu Gly Phe Leu Gly
 545 550

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 <213> *Oryctolagus cuniculus*

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 cgctgcgccc ccgggggggg ggagggcgag gaggcgggca gcggcgagg gaggggagcc 180
 ggggaggggg gcgcccgcgt gggagggagg cagcgcgcac ggtgcagccg ggccggggcg 240
 gaggc atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc 290
 Met Ala Gly Pro Pro Ala Leu Pro Pro Glu Thr Ala Ala Ala
 1 5 10 15

 gcc acc acg gcc gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac 338
 Ala Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His
 20 25 30

 tac caa gag tgg att ctg gac acc atc gac tcg ctg cgc tcg cgc aag 386
 Tyr Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys
 35 40 45

 gcg cgg ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac 434
 Ala Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His
 50 55 60

 ggc ccg gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag 482
 Gly Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln
 65 70 75

 cag cgc gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc 530
 Gln Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg
 80 85 90 95

 aac gcg gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc 578
 Asn Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala
 100 105 110

"TCTT" 62552001

ccg ccg cgc gcc ccc cgc ggg ggc ccc gcc gcc gcc gcc gcg ccg ccg Pro Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Ala Pro Pro 115 120 125	626
ccc acg ccc gcc ccg ccg ccg ccg ccc gcg ccc gtc gcc gcc gcc gcc Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala 130 135 140	674
gcc ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gct gcc gcc aca Ala Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Ala Thr 145 150 155	722
gcg ccc ccc tcg ccc ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg Ala Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg 160 165 170 175	770
gcc gcg ccc ctg gcc gcg ccg ccg ccc gcg ccc gcc gct ccc ccg gcg Ala Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala 180 185 190	818
gcg gcg ccc ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gcc gcc Ala Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala 195 200 205	866
gtc gcc gcc ccg gag tcg ccg ctg ccg ccg cca cag ccg ccg gcg Val Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala 210 215 220	914
ccg cca cag cag cag cag cag ccg ccg ccg cca ccg ccg ccg cag cag Pro Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Gln 225 230 235	962
cca cag ccg ccg ccg gag ggg ggc gcg gcg ccg gcc ggc ggc ccg gcg Pro Gln Pro Pro Pro Glu Gly Gly Ala Ala Arg Ala Gly Gly Pro Ala 240 245 250 255	1010
ccg ccc gtg agc ctg ccg gaa gtc gtg cgc tac ctc ggg ggt agc agc Arg Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser 260 265 270	1058
ggc gct ggc ggc cgc ctg acc cgc ggc cgc gtg cag ggt ctg ctg gaa Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu 275 280 285	1106
gag gag gcg gcg gcg ccg ggc cgc ctg gag cgc acc cgt ctc gga gcg Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala 290 295 300	1154
ctt gcg ctg ccc cgc ggg gac agg ccc gga ccg gcg cca ccg gcc gcc Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala 305 310 315	1202
agc gcc cgc gcg gcg ccg aac aag aga gct ggc gag gag cga gtg ctt Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu 320 325 330 335	1250

T02T 625200T

gaa aag gag gag gag gag gag gag gag gaa gac gac gag gac gac gac Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp 340 345 350	1298
gac gac gtc gtg tcc gag ggc tcg gag gtg ccc gag agc gat cgt ccc Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro 355 360 365	1346
gcg ggt gcg cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg cag Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln 370 375 380	1394
acc gcc aag gag cgg gcc aag gag tgg tcg ctg tgt ggc ccc cac cct Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro 385 390 395	1442
ggc cag gag gaa ggg cgg ggg ccg gcc gcg ggc agt ggc acc cgc cag Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln 400 405 410 415	1490
gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser 420 425 430	1538
acc acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys 435 440 445	1586
cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly 450 455 460	1634
cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val 465 470 475	1682
gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe 480 485 490 495	1730
cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr 500 505 510	1778
gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile 515 520 525	1826
tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp 530 535 540	1874
gac ccg gaa ggc ttc ctg gga tgagcacaga gccgccgcgc cccttgcccc Asp Pro Glu Gly Phe Leu Gly 545 550	1925
cacccccacc ccgcctggac ccattcctgc ctccatgtca cccaaggtgt ccagaggcc	1985

10023529 12101

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cacccctccc	ggagcctgga	tgctgcctgg	gactctggcc	tgctcatttt	gccccagat	2165
cagccccctc	cctccctcct	gtcccaggac	atttttttaa	agaaaaaaag	gaaaaaaaaa	2225
aattggggag	ggggctggga	aggtgcccc	agatcctcct	cggcccaacc	aggtgtttat	2285
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tgggaatggg	aggaggggtg	gaccttgggt	ctgtctccca	ccctctctcc	cggtgtttct	2465
gttgctcgct	cagctggctg	tattgctttt	taatatgtca	ccgaagggtt	gttttttttt	2525
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<211> 12619

<212> DNA

<213> Homo sapiens

<400> 49

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tagaaacacg	ttgagtacct	attatgtact	aggcacttag	atcattgtga	gacaataaaa	180
aatactgcat	tagaaaagga	cattttttcac	atcttaaatg	caataagcat	tatttggtcg	240
gcagtttaatt	acattttaaca	cattaaacat	atagagcaaa	attctgagca	atcaaaataa	300
ttataccctt	gagcaatcga	ttattttaaat	ttctttcact	attcccttaa	gctgatttct	360
actctgggat	ttcttcatag	ttctcaaata	agaaaataaa	aaatttccta	aataaggcaa	420
tacaaaagaa	tagaaatgta	agagaagaga	tattattagct	cttgaatccc	tgtttccatt	480
tgctgtcaat	agtgcctcta	atgttcgatt	ttctcttcaa	agaaaaatct	tgatttaaaa	540
ggaagaaaaa	gtacaatcac	ctttaacagc	taaagtatac	tgatttagcat	ctactaaagt	600
tagcaaagac	tgaaactgaa	aaaaaattgt	aaaatcttta	ttctaagtta	tataacgcca	660
ttcaccatag	taatgatttt	atactttggt	atatggcttt	ttaaaataaa	tattgccaac	720
aggtaaaaaat	ttttcctttg	ctgtcttaag	gcattcctaa	gagaattttt	accagtgtgt	780
gttcataact	tgaatgttaa	tttaaacaat	gttacttcta	tcacctaaat	gatatactta	840
tagaagagtg	gtttaattgg	gaacagaaaa	acaccacatt	gcttcttccc	aagaaaaagg	900
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